

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bander, Neil H.
- (ii) TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF
PROSTATE CANCER
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 - (B) STREET: Clinton Square, P.O. Box 1051
 - (C) CITY: Rochester
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 14603-1051
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/016,976
 - (B) FILING DATE: 06-MAY-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 06/022,125
 - (B) FILING DATE: 18-JUL-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Goldman, Michael L.
 - (B) REGISTRATION NUMBER: 30,727
 - (C) REFERENCE/DOCKET NUMBER: 19603/1172
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (716) 263-1304
 - (B) TELEFAX: (716) 263-1600

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTCCTGTCA GGAAGTGCAG GTGTCCTCTC TGAGGTCCAG CTGCAACAGT CTGGACCTGA	60
ACTGGTGAAG CCTGGGACTT CAGTGAGGAT ATCCTGCAAG ACTTCTGGAT ACACATTCAC	120
TGAATATACC ATACACTGGG TGAAGCAGAG CCATGGAAAG AGCCTTGAGT GGATTGGAAA	180
CATCAATCCT AACAAATGGTG GTACCACCTA CAATCAGAAG TTCGAGGACA AGGCCACATT	240
GACTGTAGAC AAGTCCTCCA GTACAGCCTA CATGGAGCTC CGCAGCCTAA CATCTGAGGA	300
TTCTGCAGTC TATTATTGTG CAGCTGGTTG GAACTTTGAC TACTGGGGCC AAGGCACCAC	360
TCTCACAGTC TCCTCAGCCA AAACGACACC C	391

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGTGTCGTT TTGGCTGAGG AGACTGTGAG AGTGGTGCCT TGGCCCCAGT AGTCAAAGTT	60
CCAACCAGCT GCACAATAAT AGACTGCAGA ATCCTCAGAT GTTAGGCTGC GGAGCTCCAT	120
GTAGGCTGTA CTGGAGGACT TGTCTACAGT CAATGTGGCC TTGTCCTCGA ACTTCTGATT	180
GTAGGTGGTA CCACCATTGT TAGGATTGAT GTTTCCAATC CACTCAAGGC TCTTTCCATG	240
GCTCTGCTTC ACCCAGTGTA TGGTATATTC AGTGAATGTG TATCCAGAAG TCTTGCAGGA	300
TATCCTCACT GAAGTCCCAG GCTTCACCAG TTCAGGTCCA GACTGTTGCA GCTGGACCTC	360
AGAGAGGACA CCTGCAGTTC CTAGCAGGAG A	391

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Ser Pro Val Arg Asn Cys Arg Cys Pro Leu Gly Pro Ala Ala Thr Val
1      5      10      15
Trp Thr Thr Gly Glu Ala Trp Asp Phe Ser Glu Asp Ile Leu Gln Asp
20      25      30
Phe Trp Ile His Ile His Ile Tyr His Thr Leu Gly Glu Ala Glu Pro.
35      40      45
Trp Lys Glu Pro Val Asp Trp Lys His Gln Ser Gln Trp Trp Tyr His
50      55      60
Leu Gln Ser Glu Val Arg Gly Gln Gly His Ile Asp Cys Arg Gln Val
65      70      75      80
Leu Gln Tyr Ser Leu His Gly Ala Pro Gln Pro Asn Ile Gly Phe Cys
85      90      95
Ser Leu Leu Leu Cys Ser Trp Leu Glu Leu Leu Leu Gly Pro Arg His
100     105     110
His Ser His Ser Leu Leu Ser Gln Asn Asp Thr
115     120

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Leu Leu Ser Gly Thr Ala Gly Val Leu Ser Glu Val Gln Leu Gln Gln
1      5      10      15
Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Arg Ile Ser Cys
20      25      30
Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His Trp Val Lys
35      40      45

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Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asn Pro Asn
50 55 60
Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe Glu Asp Lys Ala Thr Leu
65 70 75 80
Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu
85 90 95
Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Gly Trp Asn Phe
100 105 110
Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
115 120 125
Thr Pro
130

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Ser Cys Gln Glu Leu Gln Val Ser Ser Leu Arg Ser Ser Cys Asn
1 5 10 15
Ser Leu Asp Leu Asn Trp Ser Leu Gly Leu Gln Gly Tyr Pro Ala Arg
20 25 30
Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala
35 40 45
Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val
50 55 60
Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser
65 70 75 80
Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu
85 90 95
Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys
100 105 110
Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro
115 120 125

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGGTCCAGC TGCAACAGTC TGGACCTGAA CTGGTGAAGC CTGGGACTTC AGTGAGGATA 60
TCCTGCAAGA CTTCTGGATA CACATTCACCT GAATATACCA TACACTGGGT GAAGCAGAGC 120
CATGGAAAGA GCCTTGAGTG GATTGGAAAC ATCAATCCTA ACAATGGTGG TACCACCTAC 180
AATCAGAAGT TCGAGGACAA GGCCACATTG ACTGTAGACA AGTCCTCCAG TACAGCCTAC 240
ATGGAGCTCC GCAGCCTAAC ATCTGAGGAT TCTGCAGTCT ATTATTGTGC AGCTGGTTGG 300
AACTTTGACT ACTGGGGCCA AGGCACCACT CTCACAGTCT CCTCA 345

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAGGAGACT GTGAGAGTGG TGCCTTGGCC CCAGTAGTCA AAGTTCCAAC CAGCTGCACA 60
ATAATAGACT GCAGAATCCT CAGATGTTAG GCTGCGGAGC TCCATGTAGG CTGTACTGGA 120
GGACTTGTCT ACAGTCAATG TGGCCTTGTC CTCGAACTTC TGATTGTAGG TGGTACCACC 180
ATTGTTAGGA TTGATGTTTC CAATCCACTC AAGGCTCTTT CCATGGCTCT GCTTCACCCA 240
GTGTATGGTA TATTCAGTGA ATGTGTATCC AGAAGTCTTG CAGGATATCC TCACTGAAGT 300
CCCAGGCTTC ACCAGTTCAG GTCCAGACTG TTGCAGCTGG ACCTC 345

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
 1 5 10 15
 Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
 20 25 30
 Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45
 Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
 50 55 60
 Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
 100 105 110
 Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTATATGGAG CTGATGGGAA CATTGTAATG ACCCAATCTC CCAAATCCAT GTCCATGTCA 60
 GTAGGAGAGA GGGTCACCTT GACCTGCAAG GCCAGTGAGA ATGTGGTTAC TTATGTTTCC 120
 TGGTATCAAC AGAAACCAGA GCAGTCTCCT AAAGTCTGTA TATACGGGGC ATCCAACCGG 180
 TACACTGGGG TCCCCGATCG CTTACAGGC AGTGGATCTG CAACAGATT CACTCTGACC 240

ATCAGCAGTG TGCAGGCTGA AGACCTTGCA GATTATCACT GTGGACAGGG TTACAGCTAT 300
CCGTACACGT TCGGAGGGGG GACCAAGCTG GAAATAAAAC GGGCTGATGC TGCACCAACT 360
GTA 363

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACAGTTGGT GCAGCATCAG CCCGTTTTAT TTCCAGCTTG GTCCCCCCTC CGAACGTGTA 60
CGGATAGCTG TAACCCTGTC CACAGTGATA ATCTGCAAGG TCTTCAGCCT GCACACTGCT 120
GATGGTCAGA GTGAAATCTG TTGCAGATCC ACTGCCTGTG AAGCGATCGG GGACCCCAGT 180
GTACCGGTTG GATGCCCCGT ATATCAGCAG TTTAGGAGAC TGCTCTGGTT TCTGTTGATA 240
CCAGGAAACA TAAGTAACCA CATTCTCACT GGCCTTGACG GTCAAGGTGA CCCTCTCTCC 300
TACTGACATG GACATGGATT TGGGAGATTG GGTCATTACA ATGTTCCCAT CAGCTCCATA 360
TAA 363

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser
1 5 10 15
Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys Ala Ser
20 25 30
Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln
35 40 45
Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln
85 90 95
Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110
Lys Arg Ala Asp Ala Ala Pro Thr Val
115 120

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro
1 5 10 15
Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu
20 25 30
Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys
35 40 45
Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln
50 55 60
Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu
65 70 75 80
Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr
85 90 95
Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln
100 105 110
Leu Tyr

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His
 1 5 10 15
 Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu
 20 25 30
 Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser
 35 40 45
 Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser
 50 55 60
 Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln
 65 70 75 80
 Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu
 85 90 95
 Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys
 100 105 110
 Cys Thr Asn Cys
 115

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC 60
 TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CCTGGTATCA ACAGAAACCA 120
 GAGCAGTCTC CTAAACTGCT GATATACGGG GCATCCAACC GGTACACTGG GGTCCCCGAT 180
 CGCTTCACAG GCAGTGGATC TGCAACAGAT TTTACTCTGA CCATCAGCAG TGTGCAGGCT 240
 GAAGACCTTG CAGATTATCA CTGTGGACAG GGTACAGCT ATCCGTACAC GTTCGGAGGG 300
 GGGACCAAGC TGGAAATAAA A 321

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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TTTTATTTCC AGCTTGGTCC CCCCTCCGAA CGTGTACGGA TAGCTGTAAC CCTGTCCACA      60
GTGATAATCT GCAAGGTCTT CAGCCTGCAC ACTGCTGATG GTCAGAGTGA AATCTGTTGC      120
AGATCCACTG CCTGTGAAGC GATCGGGGAC CCCAGTGTAC CGGTTGGATG CCCC GTATAT      180
CAGCAGTTTA GGAGACTGCT CTGGTTTCTG TTGATACCAG GAAACATAAG TAACCACATT      240
CTCACTGGCC TTGCAGGTCA AGGTGACCCT CTCTCCTACT GACATGGACA TGGATTGGG      300
AGATTGGGTC ATTACAATGT T      321

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(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1           5           10           15
Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
20           25           30
Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
35           40           45
Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50           55           60
Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
65           70           75           80
Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr
85           90           95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100          105

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACATTGTGA TGACCCAGTC TCACAAATTC ATGTCCACAT CAGTAGGAGA CAGGGTCAGC	60
ATCATCTGTA AGGCCAGTCA AGATGTGGGT ACTGCTGTAG ACTGGTATCA ACAGAAACCA	120
GGACAATCTC CTAAACTACT GATTTATTGG GCATCCACTC GGCACACTGG AGTCCCTGAT	180
CGCTTCACAG GCAGTGGATC TGGGACAGAC TTCACTCTCA CCATTACTAA TGTTCAGTCT	240
GAAGACTTGG CAGATTATTT CTGTCAGCAA TATAACAGCT ATCCTCTCAC GTTCGGTGCT	300
GGGACCATGC TGGACCTGAA A	321

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTCAGGTCC AGCATGGTCC CAGCACCGAA CGTGAGAGGA TAGCTGTTAT ATTGCTGACA	60
GAAATAATCT GCCAAGTCTT CAGACTGAAC ATTAGTAATG GTGAGAGTGA AGTCTGTCCC	120
AGATCCACTG CCTGTGAAGC GATCAGGGAC TCCAGTGTGC CGAGTGGATG CCAATAAAT	180
CAGTAGTTTA GGAGATTGTC CTGGTTTCTG TTGATACCAG TCTACAGCAG TACCCACATC	240
TTGACTGGCC TTACAGATGA TGCTGACCCT GTCTCCTACT GATGTGGACA TGAATTTGTG	300
AGACTGGGTC ATCACAATGT C	321

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15
Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
20 25 30
Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45
Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser
65 70 75 80
Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95
Thr Phe Gly Ala Gly Thr Met Leu Asp Leu Lys
100 105